

GenCore version 4.5
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OM protein -- protein search, using sw model

Run on: June 28, 2001, 15:54:35 ; Search time 105.36 Seconds
(without alignments)
36.089 Million cell updates/sec

Title: US-09-724-406-10
Perfect score: 587
Sequence: 1 DIVLTQSPASLAVSLGQRAT.....COQSNEDPWFPGSGTKLEIK 111

Scoring table:

BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	574	97.8	111	1	P01669 mus musculu
2	571	97.3	111	1	P01667 mus musculu
3	565	96.3	111	1	P01665 mus musculu
4	560	95.4	111	1	P01666 mus musculu
5	550.5	93.8	110	1	P01668 mus musculu
6	548	93.4	111	1	P01664 mus musculu
7	502	85.5	111	1	P01670 mus musculu
8	501	85.3	131	1	P01671 mus musculu
9	499	85.0	111	1	P01672 mus musculu
10	495	84.3	111	1	P01673 mus musculu
11	494	84.0	111	1	P01674 mus musculu
12	493	84.0	111	1	P01675 mus musculu
13	492	83.8	111	1	P01676 mus musculu
14	490	83.5	111	1	P01677 mus musculu
15	480	81.8	111	1	P01678 mus musculu
16	476	81.1	111	1	P01679 mus musculu
17	472.5	80.5	112	1	P01680 mus musculu
18	471	80.2	111	1	P01681 mus musculu
19	469	79.9	112	1	P01682 mus musculu
20	468	79.7	112	1	P01683 mus musculu
21	454	77.3	108	1	P01684 mus musculu
22	442	75.3	111	1	P01685 mus musculu
23	406	69.2	114	1	P01686 mus musculu
24	398	67.8	114	1	P01687 mus musculu
25	391.5	66.7	133	1	P01688 mus musculu
26	386	65.8	108	1	P01689 mus musculu
27	375.5	64.0	133	1	P01690 mus musculu
28	374.5	63.8	129	1	P01691 mus musculu
29	374	63.7	129	1	P01692 mus musculu
30	372	63.4	108	1	P01693 mus musculu
31	372	63.4	108	1	P01694 mus musculu
32	371.5	63.3	129	1	P01695 mus musculu
33	371	63.2	108	1	P01696 mus musculu

34	371	63.2	108	1	KV1M_HUMAN	P01605 homo sapien
35	371	63.2	108	1	KV1Y_HUMAN	P01606 homo sapien
36	365.5	62.3	129	1	KV3L_HUMAN	P01607 homo sapien
37	363	61.8	108	1	KV1K_HUMAN	P01608 homo sapien
38	363	61.8	108	1	KV1N_HUMAN	P01609 homo sapien
39	362.5	61.8	113	1	KV2G_MOUSE	P01610 mus musculu
40	362	61.7	108	1	KV1P_HUMAN	P01611 mus musculu
41	361.5	61.6	107	1	KV6A_MOUSE	P01612 mus musculu
42	361.5	61.6	109	1	KV3B_HUMAN	P01613 mus musculu
43	361.5	61.6	109	1	KV3D_HUMAN	P01614 mus musculu
44	358	61.0	108	1	KV1R_HUMAN	P01615 mus musculu
45	358	61.0	108	1	KV1R_HUMAN	P01616 mus musculu

ALIGNMENTS

RESULT	ID	STANDARD	PRT	111 AA
1	KV3Q_MOUSE			
2	KV3Q_MOUSE			
3	P01669			
4	21-JUL-1986 (Rel. 01, Created)			
5	21-JUL-1986 (Rel. 01, Last sequence update)			
6	15-JUL-1999 (Rel. 38, Last annotation update)			
7	IG KAPPA CHAIN V-III REGION PC 7769.			
8	Mus musculus (Mouse).			
9	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
10	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murine; Mus.			
11	NCBI TaxID=10090;			
12	SEQUENCE			
13	MEDLINE=79073152; PubMed=103003;			
14	Weigert M., Gattalitan L., Loh E., Schilling J., Hood L.E.;			
15	"Rearrangement of genetic information may produce immunoglobulin			
16	diversity."			
17	Nature 276:785-790(1978).			
18	PIR: E01937; KVM565.			
19	InterPro: IPR003006;			
20	PIR: P00047; I9: 1.			
21	Immunoglobulin V region.			
22	DOMAIN 1			
23	DOMAIN 2			
24	DOMAIN 3			
25	DOMAIN 4			
26	DOMAIN 5			
27	DOMAIN 6			
28	DOMAIN 7			
29	DOMAIN 8			
30	DOMAIN 9			
31	DOMAIN 10			
32	DOMAIN 11			
33	DOMAIN 12			
34	DOMAIN 13			
35	DOMAIN 14			
36	DOMAIN 15			
37	DOMAIN 16			
38	DOMAIN 17			
39	DOMAIN 18			
40	DOMAIN 19			
41	DOMAIN 20			
42	DOMAIN 21			
43	DOMAIN 22			
44	DOMAIN 23			
45	DOMAIN 24			

Query Match 97.8%; Score 574; DB 1; Length 111;
Best local similarity 97.3%; Pred. No. 2.3e-51;
Matches 108; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY	1	DIVLTQSPASLAVSLGQRATISCKASQSYDFDGSYNNYQKPGQPVLYTAASTLES	60
DB	1	DIVLTQSPASLAVSLGQRATISCKASQSYDFDGSYNNYQKPGQPVLYTAASTLES	60
OY	61	GTPARSSGSGTDFLTNHPVEEDATATYCOQSNEDPWFPGSGTKLEIK	111
DB	61	GTPARSSGSGTDFLTNHPVEEDATATYCOQSNEDPWFPGSGTKLEIK	111

RESULT 2
KV3Q_MOUSE STANDARD; PRT; 111 AA.
AC P01667;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
IG KAPPA CHAIN V-III REGION PC 6308.